

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/527,061
Source: IFWP
Date Processed by STIC: 06/20/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 06/20/2006

PATENT APPLICATION: US/10/527,061

TIME: 13:37:18

Input Set : A:\266811US0XPCT.ST25.txt

Output Set: N:\CRF4\06202006\J527061.raw

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3 <110> APPLICANT: May, Oliver
4     Buchholz, Stefan
5     Schwarm, Michael
6     Drauz, Karlheinz
7     Turner, Robert
8     Fotheringham, Ian
10 <120> TITLE OF INVENTION: MUTANTS FOR THE PREPARATION OF D-AMINO ACIDS
12 <130> FILE REFERENCE: 266811US0XPCT
14 <140> CURRENT APPLICATION NUMBER: 10/527,061
15 <141> CURRENT FILING DATE: 2005-03-09
17 <150> PRIOR APPLICATION NUMBER: PCT/EP03/11432
18 <151> PRIOR FILING DATE: 2003-10-15
20 <150> PRIOR APPLICATION NUMBER: DE 102 51 184.5
21 <151> PRIOR FILING DATE: 2002-11-04
23 <160> NUMBER OF SEQ ID NOS: 8
25 <170> SOFTWARE: PatentIn version 3.3
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 948
29 <212> TYPE: DNA
30 <213> ORGANISM: Arthrobacter crystallopoietes
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(948)
37 <400> SEQUENCE: 1
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40 1          5          10          15
42 agt tcg gaa tca aga ccc gaa gtc gtc gcc cgc ttg att gcc ctg ctg      96
43 Ser Ser Glu Ser Arg Pro Glu Val Val Ala Arg Leu Ile Ala Leu Leu
44 20          25          30
46 gaa gaa gca gct tcc cag ggc gcg gaa ctg gtg gtc ttt ccc gaa ctc      144
47 Glu Glu Ala Ala Ser Gln Gly Ala Glu Leu Val Val Phe Pro Glu Leu
48 35          40          45
50 acg ctg acc acg ttc ttc ccg cgt acc tgg ttc gaa gaa ggc gac ttc      192
51 Thr Leu Thr Thr Phe Phe Pro Arg Thr Trp Phe Glu Glu Gly Asp Phe
52 50          55          60
54 gag gaa tac ttc gat aaa tcc atg ccc aat gac gac gtc gcg ccc ctt      240
55 Glu Glu Tyr Phe Asp Lys Ser Met Pro Asn Asp Asp Val Ala Pro Leu
56 65          70          75          80
58 ttc gaa cgc gcc aaa gac ctt ggc gtg ggc ttc tac ctc gga tac gcg      288
59 Phe Glu Arg Ala Lys Asp Leu Gly Val Gly Phe Tyr Leu Gly Tyr Ala
60 85          90          95
62 gaa ctg acc agt gat gag aag cgg tac aac aca tca att ctg gtg aac      336

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63 Glu Leu Thr Ser Asp Glu Lys Arg Tyr Asn Thr Ser Ile Leu Val Asn
64      100      105      110
66 aag cac ggc gac atc gtc ggc aag tac cgc aag atg cat ctg ccg ggc      384
67 Lys His Gly Asp Ile Val Gly Lys Tyr Arg Lys Met His Leu Pro Gly
68      115      120      125
70 cac gcc gat aac cgg gaa gga cta ccc aac cag cac ctt gaa aag aaa      432
71 His Ala Asp Asn Arg Glu Gly Leu Pro Asn Gln His Leu Glu Lys Lys
72      130      135      140
74 tac ttc cgc gaa gga gat ctc gga ttc ggt gtc ttc gac ttc cac ggc      480
75 Tyr Phe Arg Glu Gly Asp Leu Gly Phe Gly Val Phe Asp Phe His Gly
76 145      150      155      160
78 gtg cag gtc gga atg tgt ctc tgc aac gac cgg cga tgg ccg gag gtc      528
79 Val Gln Val Gly Met Cys Leu Cys Asn Asp Arg Arg Trp Pro Glu Val
80      165      170      175
82 tac cgc tct ttg gcc ctg cag gga gca gag ctc gtc gtc ctg ggc tac      576
83 Tyr Arg Ser Leu Ala Leu Gln Gly Ala Glu Leu Val Val Leu Gly Tyr
84      180      185      190
86 aac acc ccc gat ttc gtt ccc ggc tgg cag gaa gag cct cac gcg aag      624
87 Asn Thr Pro Asp Phe Val Pro Gly Trp Gln Glu Glu Pro His Ala Lys
88      195      200      205
90 atg ttc acg cac ctt ctt tca ctt cag gca ggg gca tac cag aac tcg      672
91 Met Phe Thr His Leu Leu Ser Leu Gln Ala Gly Ala Tyr Gln Asn Ser
92      210      215      220
94 gta ttt gtg gcg gct gcc ggc aag tcg ggc ttc gaa gac ggg cac cac      720
95 Val Phe Val Ala Ala Ala Gly Lys Ser Gly Phe Glu Asp Gly His His
96 225      230      235      240
98 atg atc ggc gga tca gcg gtc gcc gcg ccc agc ggc gaa atc ctg gca      768
99 Met Ile Gly Gly Ser Ala Val Ala Ala Pro Ser Gly Glu Ile Leu Ala
100      245      250      255
102 aaa gca gcc ggc gag ggc gat gaa gtc gtc gtt gtg aaa gca gac atc      816
103 Lys Ala Ala Gly Glu Gly Asp Glu Val Val Val Val Lys Ala Asp Ile
104      260      265      270
106 gac atg ggc aag ccc tat aag gaa agc gtc ttc gac ttc gcc gcc cat      864
107 Asp Met Gly Lys Pro Tyr Lys Glu Ser Val Phe Asp Phe Ala Ala His
108      275      280      285
110 cgg cgc ccc gac gca tac ggc atc atc gcc gaa agg aaa ggg cgg ggc      912
111 Arg Arg Pro Asp Ala Tyr Gly Ile Ile Ala Glu Arg Lys Gly Arg Gly
112      290      295      300
114 gcc cca ctg ccc gtc ccg ttc aac gtg aat gac taa      948
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120 <211> LENGTH: 315
121 <212> TYPE: PRT
122 <213> ORGANISM: Arthrobacter crystallopoietes
124 <400> SEQUENCE: 2
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130 Ser Ser Glu Ser Arg Pro Glu Val Val Ala Arg Leu Ile Ala Leu Leu

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134 Glu Glu Ala Ala Ser Gln Gly Ala Glu Leu Val Val Phe Pro Glu Leu
135          35          40          45
138 Thr Leu Thr Thr Phe Phe Pro Arg Thr Trp Phe Glu Gly Asp Phe
139          50          55          60
142 Glu Glu Tyr Phe Asp Lys Ser Met Pro Asn Asp Asp Val Ala Pro Leu
143 65          70          75          80
146 Phe Glu Arg Ala Lys Asp Leu Gly Val Gly Phe Tyr Leu Gly Tyr Ala
147          85          90          95
150 Glu Leu Thr Ser Asp Glu Lys Arg Tyr Asn Thr Ser Ile Leu Val Asn
151          100         105         110
154 Lys His Gly Asp Ile Val Gly Lys Tyr Arg Lys Met His Leu Pro Gly
155          115         120         125
158 His Ala Asp Asn Arg Glu Gly Leu Pro Asn Gln His Leu Glu Lys Lys
159          130         135         140
162 Tyr Phe Arg Glu Gly Asp Leu Gly Phe Gly Val Phe Asp Phe His Gly
163 145          150         155         160
166 Val Gln Val Gly Met Cys Leu Cys Asn Asp Arg Arg Trp Pro Glu Val
167          165         170         175
170 Tyr Arg Ser Leu Ala Leu Gln Gly Ala Glu Leu Val Val Leu Gly Tyr
171          180         185         190
174 Asn Thr Pro Asp Phe Val Pro Gly Trp Gln Glu Glu Pro His Ala Lys
175          195         200         205
178 Met Phe Thr His Leu Leu Ser Leu Gln Ala Gly Ala Tyr Gln Asn Ser
179          210         215         220
182 Val Phe Val Ala Ala Ala Gly Lys Ser Gly Phe Glu Asp Gly His His
183 225          230         235         240
186 Met Ile Gly Gly Ser Ala Val Ala Ala Pro Ser Gly Glu Ile Leu Ala
187          245         250         255
190 Lys Ala Ala Gly Glu Gly Asp Glu Val Val Val Val Lys Ala Asp Ile
191          260         265         270
194 Asp Met Gly Lys Pro Tyr Lys Glu Ser Val Phe Asp Phe Ala Ala His
195          275         280         285
198 Arg Arg Pro Asp Ala Tyr Gly Ile Ile Ala Glu Arg Lys Gly Arg Gly
199          290         295         300
202 Ala Pro Leu Pro Val Pro Phe Asn Val Asn Asp
203 305          310         315
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207 <211> LENGTH: 1404
208 <212> TYPE: DNA
209 <213> ORGANISM: Arthrobacter crystallopoietes
212 <220> FEATURE:
213 <221> NAME/KEY: CDS
214 <222> LOCATION: (1)..(1404)
216 <400> SEQUENCE: 3
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219 1          5          10          15
221 aaa atc cga gcc gac gtg ctg att gaa aac ggc aaa gtc gcc gct gtc      96

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222	Lys	Ile	Arg	Ala	Asp	Val	Leu	Ile	Glu	Asn	Gly	Lys	Val	Ala	Ala	Val	
223				20					25					30			
225	ggc	atg	ctg	gac	gcc	gcg	acg	ccg	gac	aca	gtt	gag	cgg	gtt	gac	tgc	144
226	Gly	Met	Leu	Asp	Ala	Ala	Thr	Pro	Pro	Asp	Thr	Val	Glu	Arg	Val	Asp	Cys
227			35					40					45				
229	gac	ggc	aaa	tac	gtc	atg	ccc	ggc	ggt	atc	gac	gtt	cac	acc	cac	atc	192
230	Asp	Gly	Lys	Tyr	Val	Met	Pro	Gly	Gly	Ile	Asp	Val	His	Thr	His	Ile	
231			50					55					60				
233	gac	tcc	ccc	ctc	atg	ggg	acc	acc	acc	gcc	gat	gat	ttt	gtc	agc	gga	240
234	Asp	Ser	Pro	Leu	Met	Gly	Thr	Thr	Thr	Ala	Asp	Asp	Phe	Val	Ser	Gly	
235	65					70					75					80	
237	acg	att	gca	gcc	gct	acc	ggc	gga	aca	acg	acc	atc	gtc	gat	ttc	gga	288
238	Thr	Ile	Ala	Ala	Ala	Thr	Gly	Gly	Thr	Thr	Thr	Ile	Val	Asp	Phe	Gly	
239					85					90					95		
241	cag	cag	ctc	gcc	ggc	aag	aac	ctg	ctg	gaa	tcc	gca	gac	gcg	cac	cac	336
242	Gln	Gln	Leu	Ala	Gly	Lys	Asn	Leu	Leu	Glu	Ser	Ala	Asp	Ala	His	His	
243				100						105				110			
245	aaa	aag	gcg	cag	ggg	aaa	tcc	gtc	att	gat	tac	ggc	ttc	cat	atg	tgc	384
246	Lys	Lys	Ala	Gln	Gly	Lys	Ser	Val	Ile	Asp	Tyr	Gly	Phe	His	Met	Cys	
247			115					120					125				
249	gtg	acg	aac	ctc	tat	gac	aat	ttc	gat	tcc	cat	atg	gca	gaa	ctg	aca	432
250	Val	Thr	Asn	Leu	Tyr	Asp	Asn	Phe	Asp	Ser	His	Met	Ala	Glu	Leu	Thr	
251			130					135					140				
253	cag	gac	gga	atc	tcc	agt	ttc	aag	gtc	ttc	atg	gcc	tac	cgc	gga	agc	480
254	Gln	Asp	Gly	Ile	Ser	Ser	Phe	Lys	Val	Phe	Met	Ala	Tyr	Arg	Gly	Ser	
255	145					150					155					160	
257	ctg	atg	atc	aac	gac	ggc	gaa	ctg	ttc	gac	atc	ctc	aag	gga	gtc	ggc	528
258	Leu	Met	Ile	Asn	Asp	Gly	Glu	Leu	Phe	Asp	Ile	Leu	Lys	Gly	Val	Gly	
259				165						170					175		
261	tcc	agc	ggt	gcc	aaa	cta	tgc	gtc	cac	gca	gag	aac	ggc	gac	gtc	atc	576
262	Ser	Ser	Gly	Ala	Lys	Leu	Cys	Val	His	Ala	Glu	Asn	Gly	Asp	Val	Ile	
263				180						185					190		
265	gac	agg	atc	gcc	gcc	gac	ctc	tac	gcc	caa	gga	aaa	acc	ggg	ccc	ggg	624
266	Asp	Arg	Ile	Ala	Ala	Asp	Leu	Tyr	Ala	Gln	Gly	Lys	Thr	Gly	Pro	Gly	
267			195					200					205				
269	acc	cac	gag	atc	gca	cgc	ccg	ccg	gaa	tcg	gaa	gtc	gaa	gca	gtc	agc	672
270	Thr	His	Glu	Ile	Ala	Arg	Pro	Pro	Glu	Ser	Glu	Val	Glu	Ala	Val	Ser	
271			210					215					220				
273	cgg	gcc	atc	aag	atc	tcc	cgg	atg	gcc	gag	gtg	ccg	ctg	tat	ttc	gtg	720
274	Arg	Ala	Ile	Lys	Ile	Ser	Arg	Met	Ala	Glu	Val	Pro	Leu	Tyr	Phe	Val	
275	225					230					235					240	
277	cat	ctt	tcc	acc	cag	ggg	gcc	gtc	gag	gaa	gta	gct	gcc	gcg	cag	atg	768
278	His	Leu	Ser	Thr	Gln	Gly	Ala	Val	Glu	Glu	Val	Ala	Ala	Ala	Gln	Met	
279				245						250					255		
281	aca	gga	tgg	cca	atc	agc	gcc	gaa	acg	tgc	acc	cac	tac	ctg	tcg	ctg	816
282	Thr	Gly	Trp	Pro	Ile	Ser	Ala	Glu	Thr	Cys	Thr	His	Tyr	Leu	Ser	Leu	
283				260						265					270		
285	agc	cgg	gac	atc	tac	gac	cag	ccg	gga	ttc	gag	ccg	gcc	aaa	gct	gtc	864
286	Ser	Arg	Asp	Ile	Tyr	Asp	Gln	Pro	Gly	Phe	Glu	Pro	Ala	Lys	Ala	Val	

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287          275          280          285
289 ctc aca cca ccg ctg cgc aca cag gaa cac cag gac gcg ttg tgg aga      912
290 Leu Thr Pro Pro Leu Arg Thr Gln Glu His Gln Asp Ala Leu Trp Arg
291          290          295          300
293 ggc att aac acc ggt gcg ctc agc gtc gtc agt tcc gac cac tgc ccc      960
294 Gly Ile Asn Thr Gly Ala Leu Ser Val Val Ser Ser Asp His Cys Pro
295 305          310          315          320
297 ttc tgc ttt gag gaa aag cag cgg atg ggg gca gat gac ttc cgg cag      1008
298 Phe Cys Phe Glu Glu Lys Gln Arg Met Gly Ala Asp Asp Phe Arg Gln
299          325          330          335
301 atc ccc aac ggc ggg ccc ggc gtg gag cac cga atg ctc gtg atg tat      1056
302 Ile Pro Asn Gly Gly Pro Gly Val Glu His Arg Met Leu Val Met Tyr
303          340          345          350
305 gag acc ggt gtc gcg gaa gga aaa atg acg atc gag aaa ttc gtc gag      1104
306 Glu Thr Gly Val Ala Glu Gly Lys Met Thr Ile Glu Lys Phe Val Glu
307          355          360          365
309 gtg act gcc gag aac ccg gcc aag caa ttc gat atg tac ccg aaa aag      1152
310 Val Thr Ala Glu Asn Pro Ala Lys Gln Phe Asp Met Tyr Pro Lys Lys
311          370          375          380
313 gga aca att gca ccg ggc tcc gat gca gac atc atc gtg gtc gac ccc      1200
314 Gly Thr Ile Ala Pro Gly Ser Asp Ala Asp Ile Ile Val Val Asp Pro
315 385          390          395          400
317 aac gga aca acc ctc atc agt gcc gac acc caa aaa caa aac atg gac      1248
318 Asn Gly Thr Thr Leu Ile Ser Ala Asp Thr Gln Lys Gln Asn Met Asp
319          405          410          415
321 tac acg ctg ttc gaa ggc ttc aaa atc cgt tgc tcc atc gac cag gtg      1296
322 Tyr Thr Leu Phe Glu Gly Phe Lys Ile Arg Cys Ser Ile Asp Gln Val
323          420          425          430
325 ttc tcg cgt ggc gac ctg atc agc gtc aaa ggc gaa tat gtc ggc acc      1344
326 Phe Ser Arg Gly Asp Leu Ile Ser Val Lys Gly Glu Tyr Val Gly Thr
327          435          440          445
329 cgc ggc cgc ggc gaa ttc atc aag cgg agc gct tgg agc cac ccg cag      1392
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334 Phe Glu Lys
335 465
338 <210> SEQ ID NO: 4
339 <211> LENGTH: 467
340 <212> TYPE: PRT
341 <213> ORGANISM: Arthrobacter crystallopoietes
343 <400> SEQUENCE: 4
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346 1          5          10          15
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353 Gly Met Leu Asp Ala Ala Thr Pro Asp Thr Val Glu Arg Val Asp Cys
354          35          40          45
357 Asp Gly Lys Tyr Val Met Pro Gly Gly Ile Asp Val His Thr His Ile

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Input Set : A:\266811US0XPCT.ST25.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8

VERIFICATION SUMMARY

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